

SEQ ID NO 89

LENGTH: 775

TYPE: PRT

ORGANISM: Pyrococcus furiosus

SEQUENCE: 89

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Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1           5           10          15
Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
          20          25          30
Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
          35          40          45
Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
          50          55          60
Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65          70          75          80
Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
          85          90          95
Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
          100         105         110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
          115         120         125
Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
          130         135         140
Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145          150          155          160
Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
          165         170         175
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
          180         185         190
Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
          195         200         205
Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
          210         215         220
Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225          230         235         240
Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
          245         250         255
His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
          260         265         270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
          275         280         285
Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
          290         295         300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305          310         315         320
Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
          325         330         335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
          340         345         350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
          355         360         365
Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
          370         375         380
Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385          390         395         400
Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
          405         410         415
His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
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BRS	L1	63480	polymerase	USPAT	2010/09/29 14:05
BRS	L2	24	11 and v93	USPAT	2010/09/29 14:05
BRS	L3	38105	11 and (valine mutation)	USPAT	2010/09/29 14:14
BRS	L4	744	11 and (valine.clm.)	USPAT	2010/09/29 14:14
BRS	L5	30	14 and polymerase.clm.	USPAT	2010/09/29 14:15
BRS	L6	40	valine adj mutation	USPAT	2010/09/29 14:28
BRS	L7	187	(valine adj mutation) or (valine adj substitution)	USPAT	2010/09/29 14:28

BRS	L8	139	l1 and l7	USPAT	2010/09/29 14:29
BRS	L9	9	l8 and polymerase .clm.	USPAT	2010/09/29 14:29
BRS	L10	11437	l1 and uracil	USPAT	2010/09/29 14:37
BRS	L11	1197	l10 and polymerase.clm.	USPAT	2010/09/29 14:37
BRS	L12	9	l5 and uracil	USPAT	2010/09/29 14:38

STN SEARCH:

(FILE 'HOME' ENTERED AT 14:53:01 ON 29 SEP 2010)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, JAPIO, BIOTECHNO' ENTERED AT 14:54:04 ON 29 SEP 2010

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L1      1669300 S POLYMERASE
L2      1 S L1 AND V93
L3      5269 S L1 AND URACIL
L4      1 S L1 AND POLYMERASE.TI.
L5      5057 S L1 AND VALINE
L6      13 S L5 AND URACIL
L7      11 DUP REM L6 (2 DUPLICATES REMOVED)
L8      11938 S L1 AND EXONUCLEASE
L9      29 S L8 AND VALINE
L10     14 DUP REM L9 (15 DUPLICATES REMOVED)

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ANSWER 10 OF 14 CAPLUS COPYRIGHT 2010 ACS on STN

AN 1999:409781 CAPLUS

DN 131:225462

TI A Single Tyrosine Prevents Insertion of Ribonucleotides in the Eukaryotic-type .phi.29 DNA Polymerase

AU Bonnin, Ana; Lazaro, Jose M.; Blanco, Luis; Salas, Margarita

CS Centro de Biologia Molecular "Severo Ochoa" (CSIC-UAM), Universidad Autonoma, Canto Blanco, Madrid, 28049, Spain

SO Journal of Molecular Biology (1999), 290(1), 241-251
CODEN: JMOBAK; ISSN: 0022-2836

PB Academic Press

DT Journal

LA English

AB Three conserved motifs (named A, B and C) have been proposed to form the polymn. active site in all classes of DNA-dependent polymerases. In eukaryotic-type (.alpha.-like) DNA polymerases, motif A is characterized by the consensus "Dx2SLYP". Mutants in .phi.29 DNA polymerase residue Tyr254 of this conserved motif had been previously shown to be affected in dNTP binding. Here, we show that a single substitution of Tyr254 into a valine residue enables the enzyme to incorporate ribonucleotide substrates, without affecting its wild-type affinity for dNTPs. Whereas the wild-type enzyme preferred dNTPs more than two million-fold over rNTPs, the mutation of Tyr254 into valine reduced the discrimination for rNTPs up to 1000-fold. In addn. to this discrimination mechanism, based on sugar selection, .phi.29 DNA polymerase is very inefficient when extending an RNA primer terminus, allowing its exonucleolytic degrdn. These results indicate that the Tyr254 of .phi.29 DNA polymerase is responsible for the discrimination against the 2'-OH group of an incoming ribonucleotide. This is the first time that the invariant tyrosine residue of motif A is

involved in ribo- vs. deoxyribonucleotide discrimination in an
eukaryotic-type DNA polymerase. (c) 1999 Academic Press.

OSC.G 36 THERE ARE 36 CAPLUS RECORDS THAT CITE THIS RECORD (36 CITINGS)

RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

SEQ ID NO 108

LENGTH: 882

TYPE: PRT

ORGANISM: Sulfolobus solfataricus

SEQUENCE: 108

Met	Thr	Lys	Gln	Leu	Thr	Leu	Phe	Asp	Ile	Pro	Ser	Ser	Lys	Pro	Ala
1				5					10					15	
Lys	Ser	Glu	Gln	Asn	Thr	Gln	Gln	Ser	Gln	Gln	Ser	Ala	Pro	Val	Glu
			20					25					30		
Glu	Lys	Lys	Val	Val	Arg	Arg	Glu	Trp	Leu	Glu	Glu	Ala	Gln	Glu	Asn
		35					40					45			
Lys	Ile	Tyr	Phe	Leu	Leu	Gln	Val	Asp	Tyr	Asp	Gly	Lys	Lys	Gly	Lys
	50					55				60					
Ala	Val	Cys	Lys	Leu	Phe	Asp	Lys	Glu	Thr	Gln	Lys	Ile	Tyr	Ala	Leu
65					70					75		93			80
Tyr	Asp	Asn	Thr	Gly	His	Lys	Pro	Tyr	Phe	Leu	Val	Asp	Leu	Glu	Pro
				85					90					95	
Asp	Lys	Val	Gly	Lys	Ile	Pro	Lys	Ile	Val	Arg	Asp	Pro	Ser	Phe	Asp
			100					105					110		
His	Ile	Glu	Thr	Val	Ser	Lys	Ile	Asp	Pro	Tyr	Thr	Trp	Asn	Lys	Phe
		115					120					125			
Lys	Leu	Thr	Lys	Ile	Val	Val	Arg	Asp	Pro	Leu	Ala	Val	Arg	Arg	Leu
	130						135					140			
Arg	Asn	Asp	Val	Pro	Lys	Ala	Tyr	Glu	Ala	His	Ile	Lys	Tyr	Phe	Asn
145					150					155					160
Asn	Tyr	Met	Tyr	Asp	Ile	Gly	Leu	Ile	Pro	Gly	Met	Pro	Tyr	Val	Val
			165					170						175	
Lys	Asn	Gly	Lys	Leu	Glu	Ser	Val	Tyr	Leu	Ser	Leu	Asp	Glu	Lys	Asp
		180						185					190		
Val	Glu	Glu	Ile	Lys	Lys	Ala	Phe	Ala	Asp	Ser	Asp	Glu	Met	Thr	Arg
	195						200					205			
Gln	Met	Ala	Val	Asp	Trp	Leu	Pro	Ile	Phe	Glu	Thr	Glu	Ile	Pro	Lys
	210					215						220			
Ile	Lys	Arg	Val	Ala	Ile	Asp	Ile	Glu	Val	Tyr	Thr	Pro	Val	Lys	Gly
225			230							235					240
Arg	Ile	Pro	Asp	Ser	Gln	Lys	Ala	Glu	Phe	Pro	Ile	Ile	Ser	Ile	Ala
			245						250					255	
Leu	Ala	Gly	Ser	Asp	Gly	Leu	Lys	Lys	Val	Leu	Val	Leu	Asn	Arg	Asn
		260					265						270		
Asp	Val	Asn	Glu	Gly	Ser	Val	Lys	Leu	Asp	Gly	Ile	Ser	Val	Glu	Arg
	275						280					285			
Phe	Asn	Thr	Glu	Tyr	Glu	Leu	Gly	Arg	Phe	Phe	Asp	Ile	Leu	Leu	
	290					295				300					
Glu	Tyr	Pro	Ile	Val	Leu	Thr	Phe	Asn	Gly	Asp	Asp	Phe	Asp	Leu	Pro
305				310						315					320
Tyr	Ile	Tyr	Phe	Arg	Ala	Leu	Lys	Leu	Gly	Tyr	Phe	Pro	Glu	Glu	Ile
			325						330					335	
Pro	Ile	Asp	Val	Ala	Gly	Lys	Asp	Glu	Ala	Lys	Tyr	Leu	Ala	Gly	Leu
			340				345						350		
His	Ile	Asp	Leu	Tyr	Lys	Phe	Phe	Asn	Lys	Ala	Val	Arg	Asn	Tyr	
	355						360					365			
Ala	Phe	Glu	Gly	Lys	Tyr	Asn	Glu	Tyr	Asn	Leu	Asp	Ala	Val	Ala	Lys
	370					375					380				
Ala	Leu	Leu	Gly	Thr	Ser	Lys	Val	Lys	Val	Asp	Thr	Leu	Ile	Ser	Phe
385					390					395					400
Leu	Asp	Val	Glu	Lys	Leu	Ile	Glu	Tyr	Asn	Phe	Arg	Asp	Ala	Glu	Ile
			405						410					415	
Thr	Leu	Gln	Leu	Thr	Thr	Phe	Asn	Asn	Asp	Leu	Thr	Met	Lys	Leu	Ile

			420						425						430		
Val	Leu	Phe	Ser	Arg	Ile	Ser	Arg	Leu	Gly	Ile	Glu	Glu	Leu	Thr	Arg		
		435					440					445					
Thr	Glu	Ile	Ser	Thr	Trp	Val	Lys	Asn	Leu	Tyr	Tyr	Trp	Glu	His	Arg		
		450					455				460						
Lys	Arg	Asn	Trp	Leu	Ile	Pro	Leu	Lys	Glu	Glu	Ile	Leu	Ala	Lys	Ser		
465					470					475					480		
Ser	Asn	Ile	Arg	Thr	Ser	Ala	Leu	Ile	Lys	Gly	Lys	Gly	Tyr	Lys	Gly		
				485					490						495		
Ala	Val	Val	Ile	Asp	Pro	Pro	Ala	Gly	Ile	Phe	Phe	Asn	Ile	Thr	Val		
			500					505					510				
Leu	Asp	Phe	Ala	Ser	Leu	Tyr	Pro	Ser	Ile	Ile	Arg	Thr	Trp	Asn	Leu		
		515					520					525					
Ser	Tyr	Glu	Thr	Val	Asp	Ile	Gln	Gln	Cys	Lys	Lys	Pro	Tyr	Glu	Val		
		530				535					540						
Lys	Asp	Glu	Thr	Gly	Glu	Val	Leu	His	Ile	Val	Cys	Met	Asp	Arg	Pro		
545					550					555					560		
Gly	Ile	Thr	Ala	Val	Ile	Thr	Gly	Leu	Leu	Arg	Asp	Phe	Arg	Val	Lys		
				565					570						575		
Ile	Tyr	Lys	Lys	Lys	Ala	Lys	Asn	Pro	Asn	Asn	Ser	Glu	Glu	Gln	Lys		
			580					585					590				
Leu	Leu	Tyr	Asp	Val	Val	Gln	Arg	Ala	Met	Lys	Val	Phe	Ile	Asn	Ala		
		595					600					605					
Thr	Tyr	Gly	Val	Phe	Gly	Ala	Glu	Thr	Phe	Pro	Leu	Tyr	Ala	Pro	Ala		
		610				615					620						
Val	Ala	Glu	Ser	Val	Thr	Ala	Leu	Gly	Arg	Tyr	Val	Ile	Thr	Ser	Thr		
625					630					635					640		
Val	Lys	Lys	Ala	Arg	Glu	Glu	Gly	Leu	Thr	Val	Leu	Tyr	Gly	Asp	Thr		
			645						650					655			
Asp	Ser	Leu	Phe	Leu	Leu	Asn	Pro	Pro	Lys	Asn	Ser	Leu	Glu	Asn	Ile		
			660					665					670				
Ile	Lys	Trp	Val	Lys	Thr	Thr	Phe	Asn	Leu	Asp	Leu	Glu	Val	Asp	Lys		
		675					680					685					
Thr	Tyr	Lys	Phe	Val	Ala	Phe	Ser	Gly	Leu	Lys	Lys	Asn	Tyr	Phe	Gly		
		690				695					700						
Val	Tyr	Gln	Asp	Gly	Lys	Val	Asp	Ile	Lys	Gly	Met	Leu	Val	Lys	Lys		
705					710					715					720		
Arg	Asn	Thr	Pro	Glu	Phe	Val	Lys	Lys	Val	Phe	Asn	Glu	Val	Lys	Glu		
			725						730					735			
Leu	Met	Ile	Ser	Ile	Asn	Ser	Pro	Asn	Asp	Val	Lys	Glu	Ile	Lys	Arg		
			740					745					750				
Lys	Ile	Val	Asp	Val	Val	Lys	Gly	Ser	Tyr	Glu	Lys	Leu	Lys	Asn	Lys		
		755					760					765</					